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1011

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RAW SEQUENCE LISTING

DATE: 10/01/2001

PATENT APPLICATION: US/09/746,311

TIME: 15:17:58

Input Set : C:\Crf3\Datahold\09543955

Output Set: N:\CRF3\10012001\I746311.raw

4 <110> APPLICANT: Little, II, Roger G.
6 <120> TITLE OF INVENTION: IDENTIFICATION OF NOVEL ANTIMICROBIAL AGENTS USING
7 METABOLIC OXIDATION-REDUCTION INDICATOR DYES
9 <130> FILE REFERENCE: 27129/36226
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/746,311
C--> 12 <141> CURRENT FILING DATE: 2001-09-10
14 <150> PRIOR APPLICATION NUMBER: 60/143,290
15 <151> PRIOR FILING DATE: 1999-07-12
17 <160> NUMBER OF SEQ ID NOS: 6
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1813
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (31)..(1491)
30 <220> FEATURE:
31 <221> NAME/KEY: mat_peptide
32 <222> LOCATION: (124)..(1491)
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36 Met Arg Glu Asn Met Ala Arg Gly
37 -30 -25
39 cct tgc aac gcg ccg aga tgg gtg tcc ctg atg gtg ctc gtc gcc ata 102
40 Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
41 -20 -15 -10
43 ggc acc gcc gtg aca gcg gcc gtc aac cct ggc gtc gtg gtc agg atc 150
44 Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
45 -5 -1 1 5
47 tcc cag aag ggc ctg gac tac gcc agc cag cag ggg acg gcc gct ctg 198
48 Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
49 10 15 20 25
51 cag aag gag ctg aag agg atc aag att cct gac tac tca gac agc ttt 246
52 Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
53 30 35 40
56 aag atc aag cat ctt ggg aag ggg cat tat agc ttc tac agc atg gac 294
57 Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp
58 45 50 55
60 atc cgt gaa ttc cag ctt ccc agt tcc cag ata agc atg gtg ccc aat 342
61 Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn
62 60 65 70
64 gtg ggc ctt aag ttc tcc atc agc aac gcc aat atc aag atc agc ggg 390
65 Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly
66 75 80 85
68 aaa tgg aag gca caa aag aga ttc tta aaa atg agc ggc aat ttt gac 438
69 Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp

ENTERED

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70	90		95		100		105	
72	ctg agc ata gaa ggc atg tcc att tcg gct gat ctg aag ctg ggc agt	486						
73	Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser							
74			110		115		120	
76	aac ccc acg tca ggc aag ccc acc atc acc tgc tcc agc tgc agc agc	534						
77	Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser							
78			125		130		135	
80	cac atc aac agt gtc cac gtg cac atc tca aag agc aaa gtc ggg tgg	582						
81	His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp							
82			140		145		150	
84	ctg atc caa ctc ttc cac aaa aaa att gag tct gcg ctt cga aac aag	630						
85	Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys							
86			155		160		165	
88	atg aac agc cag gtc tgc gag aaa gtg acc aat tct gta tcc tcc aag	678						
89	Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys							
90	170		175		180		185	
92	ctg caa cct tat ttc cag act ctg cca gta atg acc aaa ata gat tct	726						
93	Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser							
94			190		195		200	
96	gtg gct gga atc aac tat ggt ctg gtg gca cct cca gca acc acg gct	774						
97	Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala							
98			205		210		215	
100	gag acc ctg gat gta cag atg aag ggg gag ttt tac agt gag aac cac	822						
101	Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Glu Asn His							
102			220		225		230	
104	cac aat cca cct ccc ttt gct cca cca gtg atg gag ttt ccc gct gcc	870						
105	His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala							
106			235		240		245	
108	cat gac cgc atg gta tac ctg ggc ctc tca gac tac ttc ttc aac aca	918						
109	His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr							
110	250		255		260		265	
112	gcc ggg ctt gta tac caa gag gct ggg gtc ttg aag atg acc ctt aga	966						
113	Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg							
114			270		275		280	
116	gat gac atg att cca aag gag tcc aaa ttt cga ctg aca acc aag ttc	1014						
117	Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe							
118			285		290		295	
120	ttt gga acc ttc cta cct gag gtg gcc aag aag ttt ccc aac atg aag	1062						
121	Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys							
122			300		305		310	
124	ata cag atc cat gtc tca gcc tcc acc ccg cca cac ctg tct gtg cag	1110						
125	Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln							
126			315		320		325	
128	ccc acc ggc ctt acc ttc tac cct gcc gtg gat gtc cag gcc ttt gcc	1158						
129	Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala							
130	330		335		340		345	
132	gtc ctc ccc aac tcc ctg gct tcc ctc ttc ctg att ggc atg cac	1206						
133	Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His							
134			350		355		360	

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136 aca act ggt tcc atg gag gtc agc gcc gag tcc aac agg ctt gtt gga 1254
137 Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly
138          365          370          375
140 gag ctc aag ctg gat agg ctg ctc ctg gaa ctg aag cac tca aat att 1302
141 Glu Leu Lys Leu Asp Arg Leu Leu Leu Glu Leu Lys His Ser Asn Ile
142          380          385          390
144 ggc ccc ttc ccg gtt gaa ttg ctg cag gat atc atg aac tac att gta 1350
145 Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val
146          395          400          405
148 ccc att ctt gtg ctg ccc agg gtt aac gag aaa cta cag aaa ggc ttc 1398
149 Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe
150 410          415          420          425
152 cct ctc ccg acg ccg gcc aga gtc cag ctc tac aac gta gtg ctt cag 1446
153 Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln
154          430          435          440
156 cct cac cag aac ttc ctg ctg ttc ggt gca gac gtt gtc tat aaa 1491
157 Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys
158          445          450          455
160 tgaaggcacc aggggtgccg ggggctgtca gccgcacctg ttctctgatgg gctgtggggc 1551
162 accggctgcc ttcccccagg gaatcctctc cagatcttaa ccaagagccc cttgcaaact 1611
164 tcttcgactc agattcagaa atgatctaaa cagcaggaaa cattattcat tggaaaagtg 1671
166 catggtgtgt attttaggga ttatgagctt ctttcaaggg ctaaggctgc agagatatatt 1731
168 cctccaggaa tcgtgtttca attgtaacca agaaatttcc atttgtgctt catgaaaaaa 1791
170 aacttctggt ttttttcatg tg 1813
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 487
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 2
179 Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val
180 -30          -25          -20
182 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
183 -15          -10          -5          -1 1
185 Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
186          5          10          15
188 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
189          20          25          30
191 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
192          35          40          45
194 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
195 50          55          60          65
197 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
198          70          75          80
200 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
201          85          90          95
203 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
204          100          105          110
206 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
207          115          120          125

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209 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
210 130                      135                      140                      145
212 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
213                      150                      155                      160
215 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
216                      165                      170                      175
218 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
219                      180                      185                      190
221 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
222                      195                      200                      205
224 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
225 210                      215                      220                      225
227 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
228                      230                      235                      240
230 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
231                      245                      250                      255
233 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
234                      260                      265                      270
236 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
237                      275                      280                      285
239 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
240 290                      295                      300                      305
242 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
243                      310                      315                      320
245 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
246                      325                      330                      335
248 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
249                      340                      345                      350
251 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
252                      355                      360                      365
254 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
255 370                      375                      380                      385
257 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
258                      390                      395                      400
260 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
261                      405                      410                      415
263 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
264                      420                      425                      430
266 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
267                      435                      440                      445
269 Gly Ala Asp Val Val Tyr Lys
270 450                      455
274 <210> SEQ ID NO: 3
275 <211> LENGTH: 10
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial
281 peptide XMP.365

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Input Set : C:\Crf3\Datahold\09543955

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283 <220> FEATURE:
284 <221> NAME/KEY: SITE
285 <222> LOCATION: (1)..(10)
286 <223> OTHER INFORMATION: Positions 1-10 are D-amino acids
288 <220> FEATURE:
289 <223> OTHER INFORMATION: The C-Terminus is Amidated
291 <400> SEQUENCE: 3
292 Lys Trp Leu Ile Gln Leu Phe His Lys Lys
293   1           5           10
296 <210> SEQ ID NO: 4
297 <211> LENGTH: 12
298 <212> TYPE: PRT
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial
303   peptide XMP.391
305 <220> FEATURE:
306 <223> OTHER INFORMATION: The C-Terminus is Amidated
308 <400> SEQUENCE: 4
310 Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
311   1           5           10
314 <210> SEQ ID NO: 5
315 <211> LENGTH: 10
316 <212> TYPE: PRT
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial
321   peptide XMP.416
323 <220> FEATURE:
324 <221> NAME/KEY: SITE
325 <222> LOCATION: (1)..(10)
326 <223> OTHER INFORMATION: Positions 1-10 are D-amino acids
328 <220> FEATURE:
329 <223> OTHER INFORMATION: The C-Terminus is Amidated
331 <220> FEATURE:
332 <223> OTHER INFORMATION: 8-amino-octanyl group; NH2-(CH2)7-CO at N-Terminus
334 <400> SEQUENCE: 5
335 Lys Trp Leu Ile Gln Leu Phe His Lys Lys
336   1           5           10
339 <210> SEQ ID NO: 6
340 <211> LENGTH: 12
341 <212> TYPE: PRT
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial
346   peptide XMP.445
348 <220> FEATURE:
349 <221> NAME/KEY: SITE
350 <222> LOCATION: (1)

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6